

Exposure Response Modeling Analyses

- Regression Trees
- Starting Values
- Variable's Inclusion/Exclusion
- Heterogeneity
- Convergence
- Goodness of Fit

Exposure Response Modeling Analyses

- Specifying Starting Points
- Tests For The Significance of Parameters
- Residual Plots
- Test For Global Minimum

use model \bar{c} constant d in event intercept not
also: use 20% higher than \bar{c} as starting pt
 $u = d + \exp(-\exp^{-\frac{1}{2}(x-\bar{c})})$ use average ~~men-smoking~~
level for non-smokers
if doesn't work, fix it. as starting value for d
(backgd)

① Choose a & d (tot exp var), linearize
for a given run, vary to a max
② NLIN
 $d-R$

Use regression tree to generate a & d
linearize things
input into Proc Reg for stepwise
then do quasi-likelihood

exposure;
gender

eliminate vars one by one using LRT.

loss function
NLIN

Use estimates from analyte information (largest value)
If use S-plot in report either use ~~estimated~~ dotted line
try to estimate a and if can't use analyte data.
if doesn't converge, then choose analyte data;
does " use what it converges to.
95% upper limit of analytes

Repeated Measures Modeling

- Model (Gender, Smk status, week)
- Covariance Structure
- Tests
- Sample Size for Main Study *Test variability to determine if diff for smk and non-smk.*
Group option on repeated
Nonparametric pairwise testing (85%)

$$\text{Biomarker} = \text{Group} + \text{Gender} + \text{Week} + \text{Other Covariates} + \text{Group*Week} + \text{Subject} + \text{Random Error}$$

Where:

Biomarker	= Biomarker from the list of Biomarkers
Group	= Smokers, Non-Smokers
Week	= Weeks when the biomarker was collected
Other Covariate	= Other covariates of interest
Group*Week	= Group by Week interaction
Subject	= Between subject error
Random Error	= Within subject error

Akaike's criterion will be used to decide on the covariance structure. The intra-subject variability and the inter-subject variability will be used in conjunction with nQuery Advisor to determine the required sample size for the main study.

Supplementary Analyses

TABLE 14.5-3
COMPARISON BETWEEN SUBJECTS EXPOSED AND SUBJECTS NOT EXPOSED TO
ENVIREMENTAL TOBACCO SMOKE WITHIN A 3 DAY PERIOD OR 3 MONTHS PERIOD BEFORE
SAMPLE COLLECTION

BIOMARKER	Statistic	Exposed	Not-exposed	P-value ^a
Cotinine (units)	N MEAN, GEO MEAN SD,SE MEDIAN MIN,MAX 5%,95%			

RAP NOTE: Biomarkers analyzed are Cotinine, combined nicotine metabolites, and 4 ABD-Hb adducts.

^aP-value from a parametric or a non-parametric test.

Supplementary Analyses

TABLE 14.-5-4
COMPARISON BETWEEN NONSMOKERS EXPOSED AND NONSMOKERS NOT EXPOSED TO
ENVIREMENTAL TOBACCO SMOKE WITHIN A 3 DAY PERIOD OR 3 MONTHS PERIOD BEFORE
SAMPLE COLLECTION

BIOMARKER	Duration	Statistic	Exposed	Not-exposed	P-value ^a
Cotinine (units)		N			
		MEAN, GEO MEAN			
		SD,SE			
		MEDIAN			
		MIN,MAX			
		5%,95%			

RAP NOTE: Biomarkers analyzed are Cotinine, combined nicotine metabolites, and 4 ABD-Hb adducts.

^aP-value from a parametric or a non-parametric test.

Supplementary Analyses

- Regression analyses will be performed to determine if a relationship exists between duration and biomarkers of exposure.
- Regression analyses will be performed to determine if a relationship exists between weighted duration and biomarkers of exposure.
- Regression analyses models will depend on the Repeated analyses results.

Supplementary Analyses

Comparison of the laboratories results:

proc mixed data=one;

class subject gender group week;

model labdiff = group gender week group*gender group*week
group*gender*week/ddfm=satterth;

repeated week/type=ar(1) sub=subject;

/* or CS or UN. The covariance structure with values of */

/* the criteria (Akaike's Information Criterion) */

/* closest to zero are most desirable */

*then look at
intercept*